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# SEQUENCE LISTING

<110> Gangolli, Esha A  
Stone, David J

<120> ENDOZEPINE-LIKE PROTEINS, POLYNUCLEOTIDES ENCODING THEM  
AND METHODS OF USING THE SAME

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Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
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Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
      50             55             60

Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
      65             70             75             80

Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
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Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
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Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
      115            120            125

Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
      130            135            140

Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr
      145            150            155            160

Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn
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Val Leu Thr Ser Ala Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu
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Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu
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Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys

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Arg Asn Asn Ser Gly	Ala Pro His Arg Glu	Lys Gly Gly Glu Thr Asp
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515

520

525

Arg Arg Lys Leu Asn  
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&lt;211&gt; 3920

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala
 35             40            45

Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr
 50             55            60

Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu
 65             70            75            80

Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg
 85             90            95

Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
100            105            110

Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met
115            120            125

Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe
130            135            140

Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr

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Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp	225		230		235	240
Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser	245		250		255	
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Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp	290		295		300	
Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu	305		310		315	320
Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr	325		330		335	
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Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val	355		360		365	
Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly	370		375		380	
Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr	385		390		395	400
Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His	405		410		415	
Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly	420		425		430	
Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln	435		440		445	
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gaaggtgatc	cagagtttgc	cgaagaatgg	ttcattccag	ccaacaaatg	aaatgatgct	240
taaattttat	agcttctata	agcaggcaac	tgaaggaccc	tgtaaacttt	caaggcctgg	300
attttgggat	cctattggaa	gatataaatg	ggatgcttgg	agttcactgg	gtgatatgac	360
caaagaggaa	gccatgattg	catatgttga	agaaatgaaa	aagattattg	aaactatgcc	420
aatgactgag	aaagttgaag	aattgctgcg	tgtcataggt	ccattttatg	aaattgtcga	480
ggacaaaaag	agtggcagga	gttctgatat	aacctcagtc	cgactggaga	aaatctctaa	540
atgtttagaa	gatcttggta	atgttctcac	ttctactcca	aacgcaaaaa	ccgttaatgg	600
taaagctgaa	agcagtgaca	gtggagccga	gtctgaggaa	gaagaggccc	aagaagaagt	660
gaaaggagca	gaacaaagtg	ataatgataa	gaaaatgatg	aagaagtcag	cagaccaataa	720
gaatttggaa	gtcattgtca	ctaattggcta	tgataaagat	ggctttgttc	aggatataca	780
gaatgacatt	catgccagtt	cttccctgaa	tggcagaagc	actgaagaag	taaagcccat	840
tgatgaaaac	ttggggcaaa	ctggaaaatc	tgctgtttgc	attcaccaag	atataaatga	900
tgatcatgtt	gaagatgtta	cagggaattca	gcatttgaca	agcgattcag	acagtgaagt	960



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ttactgtgat tctatggaac aatttggaca agaagagtct ttagacagct ttacgtccaa 1020
caatggacca tttcagtatt acttgggtgg tcattccagt caacccatgg aaaattctgg 1080
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tgcagttgaa ggaaaaggtg aagtcaagca tggaggagaa gatggcagga ataacagcgg 1200
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tcagcccacc tcacagagac catcttggtg gcccttcgag atgtctcctg gtgtgctaac 1560
gtttgccatc atatggcctt ttattgcaca gtggttggtg tatttatact atcaaagaag 1620
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<210> 10  
 <211> 534  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys  
 1 5 10 15  
 Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu  
 20 25 30  
 Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala  
 35 40 45  
 Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro Thr  
 50 55 60  
 Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu  
 65 70 75 80  
 Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg  
 85 90 95  
 Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu  
 100 105 110  
 Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met  
 115 120 125  
 Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe  
 130 135 140  
 Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr  
 145 150 155 160  
 Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn  
 165 170 175  
 Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu  
 180 185 190  
 Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu



195	200	205
Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys 210 215 220		
Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp 225 230 235 240		
Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser 245 250 255		
Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn 260 265 270		
Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile Asn 275 280 285		
Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp 290 295 300		
Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu 305 310 315 320		
Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr 325 330 335		
Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg Glu 340 345 350		
Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val 355 360 365		
Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly 370 375 380		
Arg Asn Asn Ser Gly Ala Leu His Arg Glu Lys Arg Gly Gly Glu Thr 385 390 395 400		
Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His 405 410 415		
Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly 420 425 430		
Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln 435 440 445		
Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val Leu 450 455 460		
Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser 465 470 475 480		
Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro 485 490 495		
Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile		



500                      505                      510  
 Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg  
           515                      520                      525

Arg Arg Arg Lys Leu Asn  
           530

<210> 11  
 <211> 89  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Acyl CoA  
           binding protein domain sequence

<400> 11  
 Leu Gln Glu Asp Phe Glu Ala Ala Ala Glu Lys Val Lys Lys Leu Lys  
       1                      5                      10                      15  
 Lys Asn Gly Pro Val Lys Pro Ser Asn Glu Glu Lys Leu Lys Leu Tyr  
                           20                      25                      30  
 Ser Leu Tyr Lys Gln Ala Thr Val Gly Asp Val Asn Thr Glu Arg Pro  
                           35                      40                      45  
 Gly Met Phe Asp Leu Lys Gly Arg Ala Lys Trp Asp Ala Trp Asn Glu  
       50                      55                      60  
 Leu Lys Gly Met Ser Lys Glu Glu Ala Met Lys Ala Tyr Ile Ala Lys  
       65                      70                      75                      80  
 Val Glu Glu Leu Ile Ala Lys Tyr Ala  
                           85

<210> 12  
 <211> 89  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Acyl CoA  
           binding protein domain sequence

<400> 12  
 Leu Gln Glu Asp Phe Glu Ala Ala Ala Glu Lys Val Lys Lys Leu Lys  
       1                      5                      10                      15  
 Lys Asn Gly Pro Val Lys Pro Ser Asn Glu Glu Lys Leu Lys Leu Tyr  
                           20                      25                      30  
 Ser Leu Tyr Lys Gln Ala Thr Val Gly Asp Val Asn Thr Glu Arg Pro  
                           35                      40                      45



Gly Met Phe Asp Leu Lys Gly Arg Ala Lys Trp Asp Ala Trp Asn Glu  
50 55 60

Leu Lys Gly Met Ser Lys Glu Glu Ala Met Lys Ala Tyr Ile Ala Lys  
65 70 75 80

Val Glu Glu Leu Ile Ala Lys Tyr Ala  
85

<210> 13  
<211> 534  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (3)...(3)  
<223> "Xaa" = "Ile", "Leu", "Val" or "Phe"

<400> 13  
Met Tyr Xaa Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys  
1 5 10 15

Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln Leu  
20 25 30

Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala  
35 40 45

Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln Pro Thr  
50 55 60

Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu  
65 70 75 80

Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg  
85 90 95

Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu  
100 105 110

Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met  
115 120 125

Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe  
130 135 140

Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr  
145 150 155 160

Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn  
165 170 175

Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu  
180 185 190



Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln Glu Glu  
 195 200 205  
 Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met Lys Lys  
 210 215 220  
 Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly Tyr Asp  
 225 230 235 240  
 Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala Ser Ser  
 245 250 255  
 Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp Glu Asn  
 260 265 270  
 Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp Ile Asn  
 275 280 285  
 Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr Ser Asp  
 290 295 300  
 Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln Glu  
 305 310 315 320  
 Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr Tyr  
 325 330 335  
 Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg Glu  
 340 345 350  
 Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln Val  
 355 360 365  
 Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp Gly  
 370 375 380  
 Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr  
 385 390 395 400  
 Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln His  
 405 410 415  
 Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp Gly  
 420 425 430  
 Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu Gln  
 435 440 445  
 Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val Leu  
 450 455 460  
 Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys Ser  
 465 470 475 480  
 Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg Pro  
 485 490 495



Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala Ile  
500 505 510

Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln Arg  
515 520 525

Arg Arg Arg Lys Leu Asn  
530

<210> 14

<211> 536

<212> PRT

<213> Homo sapiens

<400> 14

Met Leu Phe Leu Ser Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys  
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Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp  
20 25 30

Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu  
35 40 45

Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln  
50 55 60

Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala  
65 70 75 80

Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile  
85 90 95

Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys  
100 105 110

Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu  
115 120 125

Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly  
130 135 140

Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp  
145 150 155 160

Ile Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu  
165 170 175

Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys  
180 185 190

Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Glu Ala Gln  
195 200 205

Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met  
210 215 220



Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly  
 225 230 235 240  
 Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala  
 245 250 255  
 Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp  
 260 265 270  
 Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp  
 275 280 285  
 Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr  
 290 295 300  
 Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly  
 305 310 315 320  
 Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln  
 325 330 335  
 Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe  
 340 345 350  
 Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met  
 355 360 365  
 Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu  
 370 375 380  
 Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly  
 385 390 395 400  
 Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met  
 405 410 415  
 Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly  
 420 425 430  
 Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn  
 435 440 445  
 Glu Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn  
 450 455 460  
 Val Leu Gln Arg Leu Gln Lys Leu Glu Met Leu Thr Ala Leu Gln Ala  
 465 470 475 480  
 Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln  
 485 490 495  
 Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe  
 500 505 510  
 Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr  
 515 520 525



Gln Arg Arg Arg Arg Lys Leu Asn  
 530 535

<210> 15  
 <211> 533  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys Cys  
 1 5 10 15

Cys Leu Ile Pro Gly Asp Arg Pro Trp Asp Arg Gly Arg Arg Trp Arg  
 20 25 30

Leu Glu Met Arg His Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala  
 35 40 45

Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro  
 50 55 60

Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr  
 65 70 75 80

Glu Gly Pro Cys Lys Leu Ser Lys Pro Gly Phe Trp Asp Pro Val Gly  
 85 90 95

Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu  
 100 105 110

Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Leu Glu Thr  
 115 120 125

Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu His Val Ile Gly Pro  
 130 135 140

Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Leu  
 145 150 155 160

Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly  
 165 170 175

Asn Val Leu Ala Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys Ala  
 180 185 190

Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Ala Ala Gln Glu  
 195 200 205

Asp Pro Lys Arg Pro Glu Pro Arg Asp Ser Asp Lys Lys Met Met Lys  
 210 215 220

Lys Ser Ala Asp His Lys Asn Leu Glu Ile Ile Val Thr Asn Gly Tyr  
 225 230 235 240

Asp Lys Asp Ser Phe Val Gln Gly Val Gln Asn Ser Ile His Thr Ser



245										250					255						
Pro	Ser	Leu	Asn	Gly	Arg	Cys	Thr	Glu	Glu	Val	Lys	Ser	Val	Asp	Glu						
			260					265					270								
Asn	Leu	Glu	Gln	Thr	Gly	Lys	Thr	Val	Val	Phe	Val	His	Gln	Asp	Val						
		275					280					285									
Asn	Ser	Asp	His	Val	Glu	Asp	Ile	Ser	Gly	Ile	Gln	His	Leu	Thr	Ser						
	290					295					300										
Asp	Ser	Asp	Ser	Glu	Val	Tyr	Cys	Asp	Ser	Met	Glu	Gln	Phe	Gly	Gln						
305				310						315					320						
Glu	Glu	Ser	Leu	Asp	Gly	Phe	Ile	Ser	Asn	Asn	Gly	Pro	Phe	Ser	Tyr						
			325						330					335							
Tyr	Leu	Gly	Gly	Asn	Pro	Ser	Gln	Pro	Leu	Glu	Ser	Ser	Gly	Phe	Pro						
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Glu	Ala	Val	Gln	Gly	Leu	Pro	Gly	Asn	Gly	Ser	Pro	Glu	Asp	Met	Gln						
		355					360					365									
Gly	Ala	Val	Val	Glu	Gly	Lys	Gly	Glu	Val	Lys	Arg	Gly	Gly	Glu	Asp						
370					375						380										
Gly	Gly	Ser	Asn	Ser	Gly	Ala	Pro	His	Arg	Glu	Lys	Arg	Ala	Gly	Glu						
385				390						395					400						
Ser	Glu	Glu	Phe	Ser	Asn	Ile	Arg	Arg	Gly	Arg	Gly	His	Arg	Met	Gln						
			405						410					415							
His	Leu	Ser	Glu	Gly	Ser	Lys	Gly	Arg	Gln	Val	Gly	Ser	Gly	Gly	Asp						
		420						425					430								
Gly	Glu	Arg	Trp	Gly	Ser	Asp	Arg	Gly	Ser	Arg	Gly	Ser	Leu	Asn	Glu						
		435					440					445									
Gln	Ile	Ala	Leu	Val	Leu	Met	Arg	Leu	Gln	Glu	Asp	Met	Gln	Asn	Val						
450					455						460										
Leu	Gln	Arg	Leu	His	Lys	Leu	Glu	Met	Leu	Ala	Ala	Ser	Gln	Ala	Lys						
465				470						475					480						
Ser	Ser	Ala	Leu	Gln	Thr	Ser	Asn	Gln	Pro	Thr	Ser	Pro	Arg	Pro	Ser						
			485						490				495								
Trp	Trp	Pro	Phe	Glu	Met	Ser	Pro	Gly	Ala	Leu	Thr	Phe	Ala	Ile	Ile						
		500						505					510								
Trp	Pro	Phe	Ile	Ala	Gln	Trp	Leu	Val	His	Leu	Tyr	Tyr	Gln	Arg	Arg						
	515						520					525									
Arg	Arg	Lys	Leu	Asn																	
530																					



<210> 16  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 16  
 ccttttgggg catgttgatc cg 22  
  
 <210> 17  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 17  
 cagttccagt agtcttcttg aggaaaacac ca 32  
  
 <210> 18  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 18  
 aggcaaatc atcaacatca ac 22  
  
 <210> 19  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 19  
 ctcagcccac ctcacagaga ccatct 26  
  
 <210> 20  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 20  
 ttagcacacc aggagacatc tc 22

<210> 21  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 21  
 aatcatcaac atcaacattg ca 22

<210> 22  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 22  
 ctcagcccac ctcacagaga ccatct 26

<210> 23  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 23  
 gttagcacac caggagacat ct 22

<210> 24  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 24



atcagaactc ctgccactct tt 22

<210> 25  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
Sequence

<400> 25  
tggacctatg acacgcagca attctt 26

<210> 26  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: PCR Primer  
Sequence

<400> 26  
atgccaatga ctgagaaagt tg 22

<210> 27  
<211> 22  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: PCR Primer  
Sequence

<400> 27  
tattacttgg gtggtcattc ca 22

<210> 28  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
Sequence

<400> 28  
caacccatgg aaaattcttg atttcg 26

<210> 29  
<211> 22



<212> DNA  
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 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 29  
 atattcccaa tgttgccatt tc 22  
  
  
 <210> 30  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 30  
 agaaaaccac aggaagaatg gt 22  
  
  
 <210> 31  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 31  
 cactttgtgg gctgcccata atcttt 26  
  
  
 <210> 32  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence  
  
 <400> 32  
 ataatgatgc ctgaacacca aa 22  
  
  
 <210> 33  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer



Sequence	
<400> 33 aggcaaaatc atcaacatca ac	22
<210> 34 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR Primer Sequence	
<400> 34 ctcagcccac ctcacagaga ccatct	26
<210> 35 <211> 22 <212> DNA <213> Artificial Sequence	
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<400> 35 ttagcacacc aggagacatc tc	22
<210> 36 <211> 20 <212> DNA <213> Artificial Sequence	
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<400> 36 gacctatgac acgcagcaat	20
<210> 37 <211> 26 <212> DNA <213> Artificial Sequence	
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<400> 37 tcttcaactt tctcagtcac tggcat	26



<210> 38  
 <211> 20  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
           Sequence  
  
 <400> 38  
 ggaagccatg attgcatatg 20  
  
 <210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
           Sequence  
  
 <400> 39  
 aggcaaaatc atcaacatca ac 22  
  
 <210> 40  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
           Sequence  
  
 <400> 40  
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 <210> 41  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: PCR Primer  
           Sequence  
  
 <400> 41  
 ttagcacacc aggagacatc tc 22  
  
 <210> 42  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence



<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 42  
 aatcatcaac atcaacattg ca 22

<210> 43  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 Sequence

<400> 43  
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